

SEQUENCE LISTING

<110> WALLACH, David
 MALININ, Nikolay
 SINHA, Indranil
 LEU, Stefan

<120> IREN PROTEIN, ITS PREPARATION AND USE

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 <141> 2002-03-04

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 Glu Ile Ala Ser Asp Ser Asp Ser Arg Val Thr Cys Leu Cys Ala Gln
 35 40 45
 Phe Glu Ala Val Leu Gln His Gly Leu Lys Arg Ser Arg Gly Leu Ala
 50 55 60
 Leu Thr Ala Ala Ala Ile Lys Gln Ala Ala Gly Phe Ala Ser Lys Thr
 65 70 75 80
 Glu Thr Glu Pro Val Phe Trp Tyr Tyr Val Lys Glu Val Leu Asn Lys
 85 90 95
 His Glu Leu Gln Arg Phe Tyr Ser Leu Arg His Ile Ala Ser Asp Val
 100 105 110
 Gly Arg Gly Arg Ala Trp Leu Arg Cys Ala Leu Asn Glu His Ser Leu
 115 120 125
 Glu Arg Tyr Leu His Met Leu Leu Ala Asp Arg Cys Arg Leu Ser Thr
 130 135 140
 Phe Tyr Glu Asp Trp Ser Phe Val Met Asp Glu Glu Arg Ser Ser Met
 145 150 155 160
 Leu Pro Thr Met Ala Ala Gly Leu Asn Ser Ile Leu Phe Ala Ile Asn
 165 170 175
 Ile Asp Asn Lys Asp Leu Asn Gly Gln Ser Lys Phe Ala Pro Thr Val
 180 185 190
 Ser Asp Leu Leu Lys Glu Ser Thr Gln Asn Val Thr Ser Leu Leu Lys
 195 200 205
 Glu Ser Thr Gln Gly Val Ser Ser Leu Phe Arg Glu Ile Thr Ala Ser
 210 215 220
 Ser Ala Val Ser Ile Leu Ile Lys Pro Glu Gln Glu Thr Asp Pro Leu
 225 230 235 240
 Pro Val Val Ser Arg Asn Val Ser Ala Asp Ala Lys Cys Lys Lys Glu
 245 250 255

Arg Lys Lys Lys Lys Lys Val Thr Asn Ile Ile Ser Phe Asp Asp Glu
 260 265 270

Glu Asp Glu Gln Asn Ser Gly Asp Val Phe Lys Lys Thr Pro Gly Ala
 275 280 285

Gly Glu Ser Ser Glu Asp Asn Ser Asp Arg Ser Ser Val Asn Ile Met
 290 295 300

Ser Ala Phe Glu Ser Pro Phe Gly Pro Asn Ser Asn Gly Ser Gln Ser
 305 310 315 320

Ser Asn Ser Trp Lys Ile Asp Ser Leu Ser Leu Asn Gly Glu Phe Gly
 325 330 335

Tyr Gln Lys Leu Asp Val Lys Ser Ile Asp Asp Glu Asp Val Asp Glu
 340 345 350

Asn Glu Asp Asp Val Tyr Gly Asn Ser Ser Gly Arg Lys His Arg Gly
 355 360 365

His Ser Glu Ser Pro Glu Lys Pro Leu Glu Gly Asn Thr Cys Leu Ser
 370 375 380

Gln Met His Ser Trp Ala Pro Leu Lys Val Leu His Asn Asp Ser Asp
 385 390 395 400

Ile Leu Phe Pro Val Ser Gly Val Gly Ser Tyr Ser Pro Ala Asp Ala
 405 410 415

Pro Leu Gly Ser Leu Glu Asn Gly Thr Gly Pro Glu Asp His Val Leu
 420 425 430

Pro Asp Pro Gly Leu Arg Tyr Ser Val Glu Ala Ser Ser Pro Gly His
 435 440 445

Gly Ser Pro Leu Ser Ser Leu Leu Pro Ser Ala Ser Val Pro Glu Ser
 450 455 460

Met Thr Ile Ser Glu Leu Arg Gln Ala Thr Val Ala Met Met Asn Arg
 465 470 475 480

Lys Asp Glu Leu Glu Glu Glu Asn Arg Ser Leu Arg Asn Leu Leu Asp
 485 490 495

Gly Glu Met Glu His Ser Ala Ala Leu Arg Gln Glu Val Asp Thr Leu
 500 505 510

Lys Arg Lys Val Ala Glu Gln Glu Glu Arg Gln Gly Met Lys Val Gln
 515 520 525

Ala Leu Ala Arg Glu Asn Glu Val Leu Lys Val Gln Leu Lys Lys Tyr
 530 535 540

Val Gly Ala Val Gln Met Leu Lys Arg Glu Gly Gln Thr Ala Glu Val
 545 550 555 560

Pro Asn Leu Trp Ser Val Asp Gly Glu Val Thr Val Ala Glu Gln Lys
 565 570 575

Pro Gly Glu Ile Ala Glu Glu Leu Ala Ser Ser Tyr Glu Arg Lys Leu
 580 585 590

Ile Glu Val Ala Glu Met His Gly Glu Leu Ile Glu Phe Asn Glu Arg
 595 600 605

Leu His Arg Ala Leu Val Ala Lys Glu Ala Leu Val Ser Gln Met Arg
 610 615 620

Gln Glu Leu Ile Asp Leu Arg Gly Pro Val Pro Gly Asp Leu Ser Gln
 625 630 635 640

Thr Ser Glu Asp Gln Ser Leu Ser Asp Phe Glu Ile Ser Asn Arg Ala
 645 650 655

Leu Ile Asn Val Trp Ile Pro Ser Val Phe Leu Arg Gly Lys Ala Ala
 660 665 670

Asn Ala Phe His Val Tyr Gln Val Tyr Ile Arg Ile Lys Asp Asp Glu
 675 680 685

Trp Asn Ile Tyr Arg Arg Tyr Thr Glu Phe Arg Ser Leu His His Lys
 690 695 700

Leu Gln Asn Lys Tyr Pro Gln Val Arg Ala Tyr Asn Phe Pro Pro Lys
 705 710 715 720

Lys Ala Ile Gly Asn Lys Asp Ala Lys Phe Val Glu Glu Arg Arg Lys
 725 730 735

Gln Leu Gln Asn Tyr Leu Arg Ser Val Met Asn Lys Val Ile Gln Met
 740 745 750

Val Pro Glu Phe Ala Ala Ser Pro Lys Lys Glu Thr Leu Ile Gln Leu
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Met Pro Phe Phe Val Asp Trp Ile Ser Leu Val Trp Lys Trp Pro Arg
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<210> 10
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 <212> DNA
 <213> Homo sapiens

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 aaggagtcca cgcaaggagt gagcagcgtg ttcagggaga tcacagcctc ctctgccatc 180
 tccatcctca tcaaacct 198

<210> 11
 <211> 198
 <212> DNA
 <213> Homo sapiens

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 aagtttgctc ccaccgtttc agacctctta aaggagtcaa cgcagaatgt gaacttgctg 120
 aaggagtcca cgcaaggagt gagcagcgtg ttcagggaga tcacagcctc ctctgccatc 180
 tccatcctca tcaaacct 198

<210> 12
 <211> 149
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (9)..(9)
 <223> n is a, c, g or t

<400> 12
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 tgaacttgct gaaggagtcc acgcaaggag tgagcagcgt gttcaggag atcacagcct 120
 cctctgccat ctccatcctc atcaaacct 149

<210> 13
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic

<220>
 <221> misc_feature

<222> (1)..(1)

<223> residue 1 is modified with acetyl

<220>

<221> misc_feature

<222> (4)..(4)

<223> residue 4 is modified with a-(4-methyl-coumaryl-7-amide)

<400> 13

Asp Glu Val Asp

1

<210> 14

<211> 4

<212> PRT

<213> Artificial

<220>

<223> synthetic

<220>

<221> misc_feature

<222> (1)..(1)

<223> residue 1 is modified with methyl ketone Ac

<220>

<221> misc_feature

<222> (4)..(4)

<223> residue 4 is modified with $\text{CH}_2\text{OC}(\text{O})-[2,6-(\text{CF}_3)_2]$

<400> 14

Tyr Val Ala Asp

1